

SEQUENCE LISTING

<110> Scott, Fred W.

<120> Recombinant Multivalent Viral Vaccine

<130> 18617.0016

<140> 08/552,369

<141> November 3, 1995

<160> 25

<210> 1

<211> 2254

<212> DNA

<213> feline panleukopenia virus

<220>

<223>

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 aga aat gaa aga gct aca gga tct ggg aac ggg tct gga ggc ggg 90
 Arg Asn Glu Arg Ala Thr Gly Ser Gly Asn Gly Ser Gly Gly Gly
 20 25 30
 ggt ggt ggt ggt tct ggg ggt gtg ggg att tct acg ggt act ttc 135
 Gly Gly Gly Gly Ser Gly Gly Val Gly Ile Ser Thr Gly Thr Phe
 35 40 45
 aat aat cag acg gaa ttt aaa ttt ttg gaa aac gga tgg gtg gaa 180
 Asn Asn Gln Thr Glu Phe Lys Phe Leu Glu Asn Gly Trp Val Glu
 50 55 60
 atc aca gca aac tca agc aga ctt gta cat tta aat atg cca gaa 225

Ile Thr Ala Asn Ser Ser Arg Leu Val His Leu Asn Met Pro Glu
65 70 75

agt gaa aat tat aaa aga gta gtt gta aat aat atg gat aaa act 270
Ser Glu Asn Tyr Lys Arg Val Val Val Asn Asn Met Asp Lys Thr
80 85 90

gca gtt aaa gga aac atg gct tta gat gac act cat gta caa att 315
Ala Val Lys Gly Asn Met Ala Leu Asp Asp Thr His Val Gln Ile
95 100 105

gta aca cct tgg tca ttg gtt gat gca aat gct tgg gga gtt tgg 360
Val Thr Pro Trp Ser Leu Val Asp Ala Asn Ala Trp Gly Val Trp
110 115 120

ttt aat cca gga gat tgg caa cta att gtt aat act atg agt gag 405
Phe Asn Pro Gly Asp Trp Gln Leu Ile Val Asn Thr Met Ser Glu
125 130 135

ttg cat tta gtt agt ttt gaa caa gaa att ttt aat gtt gtt tta 450
Leu His Leu Val Ser Phe Glu Gln Glu Ile Phe Asn Val Val Leu
140 145 150

aag act gtt tca gaa tct gct act cag cca cca act aaa gtt tat 495
Lys Thr Val Ser Glu Ser Ala Thr Gln Pro Pro Thr Lys Val Tyr
155 160 165

aat aat gat tta act gca tca ttg atg gtt gca tta gat agt aat 540
Asn Asn Asp Leu Thr Ala Ser Leu Met Val Ala Leu Asp Ser Asn
170 175 180

aat act atg cca ttt act cca gca gct atg aga tct gag aca ttg 585
Asn Thr Met Pro Phe Thr Pro Ala Ala Met Arg Ser Glu Thr Leu
185 190 195

ggt ttt tat cca tgg aaa cca acc ata cca act cca tgg aga tat 630
Gly Phe Tyr Pro Trp Lys Pro Thr Ile Pro Thr Pro Trp Arg Tyr
200 205 210

tat ttt caa tgg gat aga aca tta ata cca tct cat act gga act 675
Tyr Phe Gln Trp Asp Arg Thr Leu Ile Pro Ser His Thr Gly Thr
215 220 225

agt ggc aca cca aca aat ata tat cat ggt aca gat cca gat gat	720
Ser Gly Thr Pro Thr Asn Ile Tyr His Gly Thr Asp Pro Asp Asp	
230 235 240	
ggt caa ttt tat act att gaa aat tct gtg cca gta cac tta cta	765
Val Gln Phe Tyr Thr Ile Glu Asn Ser Val Pro Val His Leu Leu	
245 250 255	
aga aca ggt gat gaa ttt gct aca gga aca ttt ttt ttt gat tgt	810
Arg Thr Gly Asp Glu Phe Ala Thr Gly Thr Phe Phe Phe Asp Cys	
260 265 270	
aaa cca tgt aga cta aca cat aca tgg caa aca aac aga gca ttg	855
Lys Pro Cys Arg Leu Thr His Thr Trp Gln Thr Asn Arg Ala Leu	
275 280 285	
ggc tta cca cca ttt cta aat tct ttg cct caa tct gaa gga gct	900
Gly Leu Pro Pro Phe Leu Asn Ser Leu Pro Gln Ser Glu Gly Ala	
290 295 300	
act aac ttt ggt gat ata gga gtt caa caa gat aaa aga cgt ggt	945
Thr Asn Phe Gly Asp Ile Gly Val Gln Gln Asp Lys Arg Arg Gly	
305 310 315	
gta act caa atg gga aat aca gac tat att act gaa gct act att	990
Val Thr Gln Met Gly Asn Thr Asp Tyr Ile Thr Glu Ala Thr Ile	
320 325 330	
atg aga cca gct gag gtt ggt tat agt gca cca tat tat tct ttt	1035
Met Arg Pro Ala Glu Val Gly Tyr Ser Ala Pro Tyr Tyr Ser Phe	
335 340 345	
gaa gcg tct aca caa ggg cca ttt aaa ata cct att gca gca gga	1080
Glu Ala Ser Thr Gln Gly Pro Phe Lys Ile Pro Ile Ala Ala Gly	
350 355 360	
cgg ggg gga gcg caa aca gat gaa aat caa gca gca gat ggt gat	1125
Arg Gly Gly Ala Gln Thr Asp Glu Asn Gln Ala Ala Asp Gly Asp	
365 370 375	
cca aga tat gca ttt ggt aga caa cat ggt caa aaa act act aca	1170
Pro Arg Tyr Ala Phe Gly Arg Gln His Gly Gln Lys Thr Thr Thr	
380 385 390	
aca gga gaa aca cct gag aga ttt aca tat ata gca cat caa gat	1215

Thr Gly Glu Thr	Pro Glu Arg Phe Thr Tyr Ile Ala His Gln Asp	395	400	405
aca gga aga tat	cca gca gga gat tgg att caa aat att aac ttt	1260		
Thr Gly Arg Tyr	Pro Ala Gly Asp Trp Ile Gln Asn Ile Asn Phe	410	415	420
aac ctt cct gta	aca aat gat aat gta ttg cta cca aca gat cca	1305		
Asn Leu Pro Val	Thr Asn Asp Asn Val Leu Leu Pro Thr Asp Pro	425	430	435
att gga ggt aaa	aca gga atc aac tat act aat ata ttt aat act	1350		
Ile Gly Gly Lys	Thr Gly Ile Asn Tyr Thr Asn Ile Phe Asn Thr	440	445	450
tat ggt cct tta	act gca tta aat aat gta cca cca gtt tat cca	1395		
Tyr Gly Pro Leu	Thr Ala Leu Asn Asn Val Pro Pro Val Tyr Pro	455	460	465
aat ggt caa att	tgg gat aaa gaa ttt gat act gac tta aaa cca	1440		
Asn Gly Gln Ile	Trp Asp Lys Glu Phe Asp Thr Asp Leu Lys Pro	470	475	480
aga ctt cat gta	aat gca cca ttt gtt tgt caa aat aat tgt cct	1485		
Arg Leu His Val	Asn Ala Pro Phe Val Cys Gln Asn Asn Cys Pro	485	490	495
ggt caa tta ttt	gta aaa gtt gcg cct aat tta aca aat gaa tat	1530		
Gly Gln Leu Phe	Val Lys Val Ala Pro Asn Leu Thr Asn Glu Tyr	500	505	510
gat cct gat gca	tct gct aat atg tca aga att gta act tac tca	1575		
Asp Pro Asp Ala	Ser Ala Asn Met Ser Arg Ile Val Thr Tyr Ser	515	520	525
gat ttt tgg tgg	aaa ggt aaa tta gta ttt aaa gct aaa cta aga	1620		
Asp Phe Trp Trp	Lys Gly Lys Leu Val Phe Lys Ala Lys Leu Arg	530	535	540
gca tct cat act	tgg aat cca att caa caa atg agt att aat gta	1665		
Ala Ser His Thr	Trp Asn Pro Ile Gln Gln Met Ser Ile Asn Val	545	550	555
gat aac caa ttt	aac tat cta cca aat aat att gga gct atg aaa	1710		

tta aga aaa ctt gtc cct ggg ttt gga aaa gca tat acc ata	1008
Leu Arg Lys Leu Val Pro Gly Phe Gly Lys Ala Tyr Thr Ile	
325 330 335	
ttc aac aag acc ttg atg gaa gcc gat gct cac tac aag tca	1050
Phe Asn Lys Thr Leu Met Glu Ala Asp Ala His Tyr Lys Ser	
340 345 350	
gtc aga act tgg aat gag atc ctc cct tca aaa ggg tgt tta	1092
Val Arg Thr Trp Asn Glu Ile Leu Pro Ser Lys Gly Cys Leu	
355 360	
aga gtt ggg ggg agg tgt cat cct cat gtg aac ggg gtg ttt	1134
Arg Val Gly Gly Arg Cys His Pro His Val Asn Gly Val Phe	
365 370 375	
ttc aat ggt ata ata tta gga cct gac ggc aat gtc tta atc	1176
Phe Asn Gly Ile Ile Leu Gly Pro Asp Gly Asn Val Leu Ile	
380 385 390	
cca gag atg caa tca tcc ctc ctc cag caa cat atg gag ttg	1218
Pro Glu Met Gln Ser Ser Leu Leu Gln Gln His Met Glu Leu	
395 400 405	
ttg gaa tcc tcg gtt atc ccc ctt gtg cac ccc ctg gca gac	1260
Leu Glu Ser Ser Val Ile Pro Leu Val His Pro Leu Ala Asp	
410 415 420	
ccg tct acc gtt ttc aag gac ggt gac gag gct gag gat ttt	1302
Pro Ser Thr Val Phe Lys Asp Gly Asp Glu Ala Glu Asp Phe	
425 430	
gtt gaa gtt cac ctt ccc gat gtg cac aat cag gtc tca gga	1344
Val Glu Val His Leu Pro Asp Val His Asn Gln Val Ser Gly	
435 440 445	
gtt gac ttg ggt ctc ccg aac tgg ggg aag tat gta tta ctg	1386
Val Asp Leu Gly Leu Pro Asn Trp Gly Lys Tyr Val Leu Leu	
450 455 460	
agt gca ggg gcc ctg act gcc ttg atg ttg ata att ttc ctg	1428
Ser Ala Gly Ala Leu Thr Ala Leu Met Leu Ile Ile Phe Leu	
465 470 475	

atg aca tgt tgt aga aga gtc aat cga tca gaa cct acg caa	1470
Met Thr Cys Cys Arg Arg Val Asn Arg Ser Glu Pro Thr Gln	
480 485 490	
 cac aat ctc aga ggg aca ggg agg gag gtg tca gtc act ccc	1512
His Asn Leu Arg Gly Thr Gly Arg Glu Val Ser Val Thr Pro	
495 500	
 caa agc ggg aag atc ata tct tca tgg gaa tca cac aag agt	1554
Gln Ser Gly Lys Ile Ile Ser Ser Trp Glu Ser His Lys Ser	
505 510 515	
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Gly Gly Glu Thr Arg Leu	
520 524	

<210> 3

<211> 44

<212> DNA

<213> P11 late promoter and leader sequence

<220>

<223>

<400>

taaaaatata gtagaatttc attttgtttt tttctatgct

<210> 4

<211> 28

<212> DNA

<213> artificial sequence

<220>

<223> forward primer

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<210> 5

<211> 28

<212> DNA

<213> artificial sequence

<220> reverse primer

<223>

<400>

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<211> 18

<212> DNA

<213> artificial sequence

<220> sequencing primer

<223>

<400>

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<210> 7

<211> 2007

<212> DNA

<213> feline calicivirus

<220>

<223>

<400> 1

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Pro His Ile Lys Leu Val Ile Asn Pro Asn Lys Phe Leu His Val	
20 25 30	

ggc ttc tgc gat aac cct tta atg tgt tgt tat cct gaa tta cta	135
Gly Phe Cys Asp Asn Pro Leu Met Cys Cys Tyr Pro Glu Leu Leu	
35 40 45	

cct gaa ttt ggc acc atg tgg gat tgt gat caa tcg cca ctc caa	180
Pro Glu Phe Gly Thr Met Trp Asp Cys Asp Gln Ser Pro Leu Gln	
50 55 60	

gtc tac ctt gag tca atc ctg ggt gat gat gaa tgg tcc tcc act	225
Val Tyr Leu Glu Ser Ile Leu Gly Asp Asp Glu Trp Ser Ser Thr	
65 70 75	

cat gaa gca att gac cca gtt gtg cca cca atg cat tgg gat gaa	270
His Glu Ala Ile Asp Pro Val Val Pro Pro Met His Trp Asp Glu	
80 85 90	

gcc gga aaa atc ttc caa cca cac cct ggc gtc ctt atg cat cac	315
Ala Gly Lys Ile Phe Gln Pro His Pro Gly Val Leu Met His His	
95 100 105	

ctc atc tgt aag gtt gca gaa gga tgg gac cca aac ctg cca ctt	360
Leu Ile Cys Lys Val Ala Glu Gly Trp Asp Pro Asn Leu Pro Leu	
110 115 120	

ttc cgc ttg gaa gcg gac gat ggt tcc atc acg aca cct gaa cag	405
Phe Arg Leu Glu Ala Asp Asp Gly Ser Ile Thr Thr Pro Glu Gln	
125 130 135	

gga aca atg gtt ggt gga gtc att gct gag ccc aac gcc caa atg	450
Gly Thr Met Val Gly Gly Val Ile Ala Glu Pro Asn Ala Gln Met	
140 145 150	

tca acc gca gct gac atg gcc act ggg aaa agt gtg gac tct gag	495
Ser Thr Ala Ala Asp Met Ala Thr Gly Lys Ser Val Asp Ser Glu	

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155	160	165	
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Trp Glu Ala Phe Phe Ser Phe His Thr	Ser Val Asn Trp Ser Thr		
170	175	180	
tct gaa act cag ggg aag ata ctc ttt	aaa caa tcc tta gga cca	585	
Ser Glu Thr Gln Gly Lys Ile Leu Phe	Lys Gln Ser Leu Gly Pro		
185	190	195	
ttg ctc aac ccc tac ctt acc cat ctt	gca aag ctg tat gtt gct	630	
Leu Leu Asn Pro Tyr Leu Thr His Leu	Ala Lys Leu Tyr Val Ala		
200	205	210	
tgg tct ggt tct gtt gat gtt agg ttt	tct att tct gga tct ggt	675	
Trp Ser Gly Ser Val Asp Val Arg Phe	Ser Ile Ser Gly Ser Gly		
215	220	225	
gtc ttt gga ggg aaa tta gct gct att	gtt gtg ccg cca gga att	720	
Val Phe Gly Gly Lys Leu Ala Ala Ile	Val Val Pro Pro Gly Ile		
230	235	240	
gat cct gtt caa agt act tca atg ctg	caa tat cct cat gtc ctc	765	
Asp Pro Val Gln Ser Thr Ser Met Leu	Gln Tyr Pro His Val Leu		
245	250	255	
ttt gat gct cgt caa gtt gaa cct gtt	atc ttt tcc att ccc gat	810	
Phe Asp Ala Arg Gln Val Glu Pro Val	Ile Phe Ser Ile Pro Asp		
260	265	270	
cta aga agc acc tta tat cac ctt atg	tct gac act gat acc aca	855	
Leu Arg Ser Thr Leu Tyr His Leu Met	Ser Asp Thr Asp Thr Thr		
275	280	285	
tcg ttg gta atc atg gtg tac aat gat	ctt att aac ccc tat gct	900	
Ser Leu Val Ile Met Val Tyr Asn Asp	Leu Ile Asn Pro Tyr Ala		
290	295	300	
aat gac tca aac tct tcg ggc tgc att	gtc act gtg gaa act aaa	945	
Asn Asp Ser Asn Ser Ser Gly Cys Ile	Val Thr Val Glu Thr Lys		
305	310	315	
ccg ggg cca gat ttc aag ttt cac ctc	tta aaa cct cct ggg tct	990	
Pro Gly Pro Asp Phe Lys Phe His Leu	Leu Lys Pro Pro Gly Ser		
320	325	330	

atg tta act cac gga tct atc cca tct gat cta atc cca aaa tca	1035
Met Leu Thr His Gly Ser Ile Pro Ser Asp Leu Ile Pro Lys Ser	
335 340 345	
tct tcg ctt tgg att gga aat cgg ttt tgg tct gac ata acc gat	1080
Ser Ser Leu Trp Ile Gly Asn Arg Phe Trp Ser Asp Ile Thr Asp	
350 355 360	
ttt gta att cgg cct ttt gtg ttc cag gca aat cga cac ttt gat	1125
Phe Val Ile Arg Pro Phe Val Phe Gln Ala Asn Arg His Phe Asp	
365 370 375	
ttc aac caa gag aca gca ggt tgg agc acc cca agg ttt cgc cca	1170
Phe Asn Gln Glu Thr Ala Gly Trp Ser Thr Pro Arg Phe Arg Pro	
380 385 390	
att act atc act atc agt gtt aag gag tca gca aag ctt ggt att	1215
Ile Thr Ile Thr Ile Ser Val Lys Glu Ser Ala Lys Leu Gly Ile	
395 400 405	
gga gtg gcc acc gac tac att gtt ccc ggc ata cca gat gga tgg	1260
Gly Val Ala Thr Asp Tyr Ile Val Pro Gly Ile Pro Asp Gly Trp	
410 415 420	
ccc gac aca aca atc cca ggt gag ttg gta cct gtt ggt gac tat	1305
Pro Asp Thr Thr Ile Pro Gly Glu Leu Val Pro Val Gly Asp Tyr	
425 430 435	
gcc atc act aat ggc acc aac aat gat atc acc aca gct gcg cag	1350
Ala Ile Thr Asn Gly Thr Asn Asn Asp Ile Thr Thr Ala Ala Gln	
440 445 450	
tac gat gca gcc act gag att aga aac aac acc aat ttc aga ggc	1395
Tyr Asp Ala Ala Thr Glu Ile Arg Asn Asn Thr Asn Phe Arg Gly	
455 460 465	
atg tac att tgt ggt tct ctt caa aga gct tgg ggg gat aag aag	1440
Met Tyr Ile Cys Gly Ser Leu Gln Arg Ala Trp Gly Asp Lys Lys	
470 475 480	
att tca aat act gct ttt atc aca acc ggc acg gtt gat gga gcc	1485
Ile Ser Asn Thr Ala Phe Ile Thr Thr Gly Thr Val Asp Gly Ala	
485 490 495	

aaa ttg ata ccc agt aat acc att gac	caa aca aaa att gcc gta	1530
Lys Leu Ile Pro Ser Asn Thr Ile Asp	Gln Thr Lys Ile Ala Val	
500	505 510	
ttc caa gac aca cat gcg aat aag cat	gtc cag acc tcg gac gac	1575
Phe Gln Asp Thr His Ala Asn Lys His	Val Gln Thr Ser Asp Asp	
515	520 525	
aca ttg gcc ctg ctt ggt tat act ggt	att ggt gag gaa gca att	1620
Thr Leu Ala Leu Leu Gly Tyr Thr Gly	Ile Gly Glu Glu Ala Ile	
530	535 540	
ggg gct gac cgc gat aga gtt gtg cga	att agc gtc ctc ccg gaa	1665
Gly Ala Asp Arg Asp Arg Val Val Arg	Ile Ser Val Leu Pro Glu	
545	550 555	
cgt ggc gca cgt ggt ggc aat cac cca	atc ttc cac aaa aac tct	1710
Arg Gly Ala Arg Gly Gly Asn His Pro	Ile Phe His Lys Asn Ser	
560	565 570	
atc aag ctt ggt tat gta att agg tcc	att gat gtg ttc aat tct	1755
Ile Lys Leu Gly Tyr Val Ile Arg Ser	Ile Asp Val Phe Asn Ser	
575	580 585	
caa att ctg cat acc tct agg caa ctt	tcc ctc aat cat tac tta	1800
Gln Ile Leu His Thr Ser Arg Gln Leu	Ser Leu Asn His Tyr Leu	
590	595 600	
ttg tcg cct gac tcc ttt gct gtc tat	agg att att gac tct aat	1845
Leu Ser Pro Asp Ser Phe Ala Val Tyr	Arg Ile Ile Asp Ser Asn	
605	610 615	
gga tcc tgg ttt gac ata ggc att gat	aat gat gga ttt tct ttt	1890
Gly Ser Trp Phe Asp Ile Gly Ile Asp	Asn Asp Gly Phe Ser Phe	
620	625 630	
gtt ggt gta tca agt att ggt aaa tta	gag ttt cct tta act gcc	1935
Val Gly Val Ser Ser Ile Gly Lys Leu	Glu Phe Pro Leu Thr Ala	
635	640 645	
tcc tac atg gga att caa ttg gca aaa	att cga ctt gcc tct aac	1980
Ser Tyr Met Gly Ile Gln Leu Ala Lys	Ile Arg Leu Ala Ser Asn	
650	655 660	
att agg agt gtg atg aca aaa tta tga	2007	

Ile Arg Ser Val Met Thr Lys Leu
665

<210> 8

<211> 582

<212> DNA

<213> artificial sequence

<220> hemagglutinin left arm

<223>

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cagtatttgg agagttttat aggaagtata tagagtagaa ccagaatttt 100
gtaaaaataa atcacatttt tatactaata tgaacaact atcogatagt 150
atattgctac tatcgatagt atatacaacc aaacctcatc ctacacagat 200
atcaaaaaaa ctaggcgatg atgctactct atcgtgtaat agaaacaata 250
cacatggata tcttgatcatg agttcttggt ataagaaacc agactccatt 300
attctcttag cagccaaaaa cgatgtcgta tactttgatg attatacagc 350
ggataaaagta tcatacgatt caccgtatga tactctagct acaattatta 400
caattaaatc attgacatct gcagatgcag gtacttatat atgcgcattc 450
tttataacat caacaaatga tacggataaa atagattatg aagaatactt 500
catagatttg gttgtaaatc cagctaagtgt atccactatt gacgcgattc 550
taccaggatc taattttctcc gtgataggta tc 582
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<211> 447

<212> DNA

<213> artificial sequence

<220> hemagglutinin right arm

<223>

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acaatatcta ctacaaaata tacaactagt gactttatag agatatttgg 150

cattgtttca	ctaattttat	tattggccgt	ggcgatttto	tgtattatat	200
tattttctgta	gtggacgggc	tcgtaaacaa	gaaacaaata	tattatagat	250
tttaactcag	ataaatgtct	ggaataatta	aatctatcgt	tttgagcgga	300
ccatctgggt	cgggcaagac	agctatagtc	aggagactct	tacaagatta	350
tggaatatata	tttggatttg	tggtatccca	taccactaga	tttcctcgtc	400
ctatggaacg	agaagggtgc	gactaccatt	acgttaacag	agaggcc	447

<210> 10

<211> 40

<212> DNA

<213> artificial sequence

<220> primer P3

<223>

<400> 1
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<210> 11

<211> 22

<212> DNA

<213> artificial sequence

<220> primer P1

<223>

<400> 1
attaaacgca aatatccatg gg 22

<210> 12

<211> 27

<212> DNA

<213> artificial sequence
<220> primer F2
<223>
<400> 1
gcggtaccct ggggttaggc gatagag 27

<210> 13
<211> 20
<212> DNA

<213> artificial sequence
<220> primer P5
<223>
<400> 1
atttctccgt gataggtatc 20

<210> 14
<211> 22
<212> DNA

<213> artificial sequence
<220> primer P5
<223>

<400> 1
ggcctctctg ttaacgtaat gg 22

<210> 15
<211> 22

<212> DNA
 <213> artificial sequence
 <220> primer P2
 <223>
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 gcgtcgaagt ttgagcatgt gc 22

<210> 16

<211> 40

<212> DNA

<213> artificial sequence

<220> primer P4

<223>

<400> 1
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<210> 17

<211> 840

<212> DNA

<213> feline infectious peritonitis virus

<220>

<223>

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 atg aag tac att ttg cta ata ctc gcg tgc ata att gca tgc gtt 96

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1				5					10					15	
tat	ggt	gaa	cgc	tac	tgt	gcc	atg	caa	gac	agt	ggc	ttg	cag	tgt	141
Tyr	Gly	Glu	Arg	Tyr	Cys	Ala	Met	Gln	Asp	Ser	Gly	Leu	Gln	Cys	
				20					25					30	
att	aat	ggc	aca	aat	tca	aga	tgt	caa	acc	tgc	ttt	gaa	cgt	ggt	186
Ile	Gln	Gly	Thr	Gln	Ser	Arg	Cys	Gln	Thr	Cys	Phe	Glu	Arg	Gly	
				35					40					45	
gat	ctt	att	tgg	cat	ctt	gct	aac	tgg	aac	ttc	agc	tgg	tct	gta	231
Asp	Leu	Ile	Trp	His	Leu	Ala	Asn	Trp	Asn	Phe	Ser	Trp	Ser	Val	
				50					55					60	
ata	ttg	att	ggt	ttt	ata	aca	gtg	tta	caa	tat	ggc	aga	cca	caa	276
Ile	Leu	Ile	Val	Phe	Ile	Thr	Val	Leu	Gln	Tyr	Gly	Arg	Pro	Gln	
				65					70					75	
ttt	agc	tgg	ctc	ggt	tat	ggc	att	aaa	atg	ctg	atc	atg	tgg	cta	321
Phe	Ser	Trp	Leu	Val	Tyr	Gly	Ile	Lys	Met	Leu	Ile	Met	Trp	Leu	
				80					85					90	
tta	tgg	cct	att	ggt	cta	gcg	ctt	acg	att	ttt	aat	gca	tac	tct	366
Leu	Trp	Pro	Ile	Val	Leu	Ala	Leu	Thr	Ile	Phe	Asn	Ala	Tyr	Ser	
				95					100					105	
gag	tac	caa	ggt	tcc	aga	tat	gta	atg	ttc	ggc	ttt	agt	ggt	gca	411
Glu	Tyr	Gln	Val	Ser	Arg	Tyr	Val	Met	Phe	Gly	Phe	Ser	Val	Ala	
				110					115					120	
ggt	gca	ggt	gta	acg	ttt	gca	ctt	tgg	atg	atg	tat	ttt	gtg	aga	456
Gly	Ala	Val	Val	Thr	Phe	Ala	Leu	Trp	Met	Met	Tyr	Phe	Val	Arg	
				125					130					135	
tct	ggt	cag	cta	tat	aga	aga	acc	aaa	tca	tgg	tgg	tct	ttt	aat	501
Ser	Val	Gln	Leu	Tyr	Arg	Axg	Thr	Lys	Ser	Trp	Trp	Ser	Phe	Asn	
				140					145					150	
cct	gag	act	aat	gca	att	ctt	tgt	ggt	aat	gca	ttg	ggt	aga	agt	546
Pro	Glu	Thr	Asn	Ala	Ile	Leu	Cys	Val	Asn	Ala	Leu	Gly	Arg	Ser	
				155					160					165	
tat	gtg	ctt	ccc	tta	gat	ggt	act	cct	aca	ggt	ggt	acc	ctt	act	591
Tyr	Val	Leu	Pro	Leu	Asp	Gly	Thr	Pro	Thr	Gly	Val	Thr	Leu	Thr	

												20													25													30
ata	cct	ttg	tca	ttc	tac	aac	ccc	att	acc	ctc	gaa	caa	gga	tct	135																							
Ile	Pro	Leu	Ser	Phe	Tyr	Asn	Phe	Ile	Thr	Leu	Glu	Gln	Glu	Ser																								
				35					40					45																								
aaa	ttt	tgg	aat	tta	tgt	ccg	aga	gac	ctt	gtt	ccc	aaa	gga	ata	180																							
Lys	Phe	Trp	Asn	Leu	Cys	Pro	Arg	Asp	Leu	Val	Pro	Lys	Gly	Ile																								
				50					55					60																								
ggt	aat	aag	gat	caa	caa	att	ggt	tat	tgg	aat	aga	cag	att	cgt	225																							
Gly	Asn	Lys	Asp	Gln	Gln	Ile	Gly	Tyr	Trp	Asn	Arg	Gln	Ile	Arg																								
				65					70					75																								
tat	cgt	att	gta	aaa	ggc	cag	cgt	aag	gaa	ctc	gct	gag	agg	tgg	270																							
Tyr	Arg	Ile	Val	Lys	Gly	Gln	Arg	Lys	Glu	Leu	Ala	Glu	Arg	Trp																								
				80					85					90																								
ttc	ttt	tac	ttc	tta	ggt	aca	gga	cct	cat	gct	gat	gct	aaa	ttc	315																							
Phe	Phe	Tyr	Phe	Leu	Gly	Thr	Gly	Phe	His	Ala	Asp	Ala	Lys	Phe																								
				95					100					105																								
aaa	gac	aag	att	gat	gga	gtc	ttc	tgg	gtt	gca	agg	gat	ggt	gcc	360																							
Lys	Asp	Lys	Ile	Asp	Gly	Val	Phe	Trp	Val	Ala	Arg	Asp	Gly	Ala																								
				110					115					120																								
atg	aac	aag	ccc	aca	acg	ctt	ggc	act	cgt	gga	acc	aat	aac	gaa	405																							
Met	Asn	Lys	Pro	Thr	Thr	Leu	Gly	Thr	Arg	Gly	Thr	Asn	Asn	Glu																								
				125					130					135																								
tcc	aaa	cca	ctg	aga	ttt	gat	ggt	aag	ata	ccg	cca	cag	ttt	cag	450																							
Ser	Lys	Pro	Leu	Arg	Phe	Asp	Gly	Lys	Ile	Pro	Pro	Gln	Phe	Gln																								
				140					145					150																								
ctt	gaa	gtg	aac	cgt	tct	agg	aac	aat	tca	agg	tct	ggt	tct	cag	495																							
Leu	Glu	Val	Asn	Arg	Ser	Arg	Asn	Asn	Ser	Arg	Ser	Gly	Ser	Gln																								
				155					160					165																								
tct	aga	tct	gtt	tca	aga	aac	aga	tct	caa	tct	aga	gga	aga	cac	540																							
Ser	Arg	Ser	Val	Ser	Arg	Asn	Arg	Ser	Gln	Ser	Arg	Gly	Arg	His																								
				170					175					180																								
cat	tcc	aat	aac	cag	aat	aat	aat	gtt	gag	gat	aca	att	gta	gcc	585																							
His	Ser	Asn	Asn	Gln	Asn	Asn	Asn	Val	Glu	Asp	Thr	Ile	Val	Ala																								
				185					190					195																								

gtg	ctt	gaa	aaa	tta	ggg	gtt	act	gac	aaa	caa	agg	tca	cgt	tct	630
Val	Leu	Glu	Lys	Leu	Gly	Val	Thr	Asp	Lys	Gln	Arg	Ser	Arg	Ser	
				200					205					210	
aaa	cct	aga	gaa	cgt	agt	gat	tcc	aaa	cct	agg	gac	aca	aca	cct	675
Lys	Pro	Arg	Glu	Arg	Ser	Asp	Ser	Lys	Pro	Arg	Asp	Thr	Thr	Pro	
				215					220					225	
aag	aat	gcc	aac	aaa	cac	acc	tgg	aag	aaa	act	gca	ggc	aag	gga	720
Lys	Asn	Ala	Asn	Lys	His	Thr	Trp	Lys	Lys	Thr	Ala	Gly	Lys	Gly	
				230					235					240	
gat	gtg	aca	act	ttc	tat	ggg	gct	aga	agt	agt	tca	gct	aac	ttt	765
Asp	Val	Thr	Thr	Phe	Tyr	Gly	Ala	Arg	Ser	Ser	Ser	Ala	Asn	Phe	
				245					250					255	
ggg	gat	agt	gat	ctc	gtt	gcc	aat	ggg	aac	gct	gcc	aaa	tcg	tac	810
Gly	Asp	Ser	Asp	Leu	Val	Ala	Asn	Gly	Asn	Ala	Ala	Lys	Cys	Tyr	
				260					265					270	
cct	cag	ata	gct	gaa	tgt	gtt	cca	tca	gtg	tct	agc	ata	atc	ttt	855
Pro	Gln	Ile	Ala	Glu	Cys	Val	Pro	Ser	Val	Ser	Ser	Ile	Ile	Phe	
				275					280					285	
ggc	agt	caa	tgg	tct	gct	gaa	gaa	gct	ggg	gat	caa	gtg	aaa	gtc	900
Gly	Ser	Gln	Trp	Ser	Ala	Glu	Glu	Ala	Gly	Asp	Gln	Val	Lys	Val	
				290					295					300	
acg	ctc	act	cac	acc	tac	tac	ctg	cca	aag	gat	gat	gcc	aaa	act	945
Thr	Leu	Thr	His	Thr	Tyr	Tyr	Leu	Pro	Lys	Asp	Asp	Ala	Lys	Thr	
				305					310					315	
agt	caa	ttc	cta	gaa	cag	att	gac	gct	tac	aag	cga	cct	tct	gaa	990
Ser	Gln	Phe	Leu	Glu	Gln	Ile	Asp	Ala	Tyr	Lys	Atg	Pro	Ser	Glu	
				320					325					330	
gtg	gct	aag	gat	cag	agg	caa	aga	aga	tcc	cgt	tct	aag	tct	gct	1035
Val	Ala	Lys	Asp	Gln	Arg	Gln	Arg	Arg	Ser	Arg	Ser	Lys	Ser	Ala	
				335					340					345	
gat	aag	aag	cct	gag	gag	ttg	tct	gta	act	ctt	gtg	gag	gca	tac	1080
Asp	Lys	Lys	Pro	Glu	Glu	Lys	Ser	Val	Thr	Leu	Val	Glu	Ala	Tyr	
				350					355					360	
aca	gat	gtg	ttt	gat	gac	aca	cag	gtt	gag	atg	att	gat	gag	gtt	1125

	80		85		90	
aac cca acc aat gta aaa cac ggg gca cgt tac tcc tcc tca aaa	365					
Asn Pro Thr Asn'Val Lys His Gly Ala Arg Tyr Ser Ser Ser Lys						
	95		100		105	
tat gga tgt aaa act aca gat aga aaa aaa cag caa cag aca tac	410					
Tyr Gly Cys Lys Thr Thr Asp Arg Lys Lys Gln Gln Gln Thr Tyr						
	110		115		120	
ccc ttt tac gtc tgc ccc gga cat gcc ccc tcg ttg ggg cca aag	455					
Pro Phe Tyr Val Cys Pro Gly His Ala Pro Ser Leu Gly Pro Lys						
	125		130		135	
gga aca cat tgt gga ggg gca caa gat ggg ttt tgt gcc gca tgg	500					
Gly Thr His Cys Gly Gly Ala Gln Asp Gly Phe Cys Ala Ala Trp						
	140		145		150	
gga tgt gag acc acc gga gaa gct tgg tgg aag ccc acc tcc tca	545					
Gly Cys Glu Thr Thr Gly Glu Thr Trp Trp Lys Pro Thr Ser Ser						
	155		160		165	
tgg gac tat atc aca gta aaa aga ggg agt agt cag gac aat agc	590					
Trp Asp Tyr Ile Thr Val Lys Arg Gly Ser Ser Gln Asp Asn Ser						
	170		175		180	
tgt gag gga aaa tgc aac ccc ctg gtt ttg cag ttc acc cag aag	635					
Cys Glu Gly Lys Cys Asn Pro Leu Val Leu Gln Phe Thr Gln Lys						
	185		190		195	
gga aga caa gcc tct tgg gac gga cct aag atg tgg gga ttg cga	680					
Gly Arg Gln Ala Ser Trp Asp Gly Pro Lys Met Trp Gly Leu Arg						
	200		205		210	
cta tac cgt aca gga tat gac cct atc gct tta ttc acg gtg tcc	725					
Leu Tyr Arg Thr Gly Tyr Asp Pro Ile Ala Leu Phe Thr Val Ser						
	215		220		225	
cgg cag gta tca acc att acg ccg cct cag gca atg gga cca aac	770					
Arg Gln Val Ser Thr Ile Thr Pro Pro Gln Ala Met Gly Pro Asn						
	230		235		240	
cta gtc tta cct gat caa aaa ccc cca tcc cga caa tct caa aca	815					
Leu Val Leu Pro Asp Gln Lys Pro Pro Ser Arg Gln Ser Gln Thr						

245	250	255	
ggg tcc aaa gtg gcg acc cag agg ccc	caa acg aat gaa agc gcc	860	
Gly Ser Lys Val Ala Thr Gln Arg Pro	Gln Thr Asn Glu Ser Ala		
260	265	270	
cca agg tct gtt gcc ccc acc acc atg	ggg ccc aaa cgg att ggg	905	
Pro Arg Ser Val Ala Pro Thr Thr Met	Gly Pro Lys Arg Ile Gly		
275	280	285	
acc gga gat agg tta ata aat tta gta	caa ggg aca tac cta gcc	950	
Thr Gly Asp Arg Leu Ile Asn Leu Val	Gln Gly Thr Tyr Leu Ala		
290	295	300	
tta aat gcc acc gac ccc aac aaa act	aaa gac tgt tgg ctc tgc	995	
Leu Asn Ala Thr Asp Pro Asn Lys Thr	Lys Asp Cys Trp Leu Cys		
305	310	315	
ctg gtt tct cga cca ccc tat tac gaa	ggg att gca atc tta ggt	1040	
Leu Val Ser Arg Pro Pro Tyr Tyr Glu	Gly Ile Ala Ile Leu Gly		
320	325	330	
acc tac agc aac caa aca aac ccc ccc	cca tcc tgc cta tct act	1085	
Asn Tyr Ser Asn Gln Thr Asn Pro Pro	Pro Ser Cys Leu Ser Ile		
335	340	345	
ccg caa cac aaa cta act ata tct gaa	gta tca ggg caa gga atg	1130	
Pro Gln His Lys Leu Thr Ile Ser Glu	Val Ser Gly Gln Gly Met		
350	355	360	
tgc ata ggg act gtt cct aaa acc cac	cag gct ttg tgc aat aag	1175	
Cys Ile Gly Thr Val Pro Lys Thr His	Gln Ala Leu Cys Asn Lys		
365	370	375	
aca caa cag gga cat aca ggg gcg cac	tat cta gcc gcc ccc aac	1220	
Thr Gln Gln Gly His Thr Gly Ala His	Tyr Leu Ala Ala Pro Asn		
380	385	390	
ggc acc tat tgg gcc tgt aac act gga	ctc acc cca tgc att tcc	1265	
Gly Thr Tyr Trp Ala Cys Asn Thr Gly	Leu Thr Pro Cys Ile Ser		
395	400	405	

atg gcg gtg ctc aat tgg acc tct gat ttt tgt gtc tta atc gaa 1310
Met Ala Val Leu Asn Trp Thr Ser Asp Phe Cys Val Leu Ile Glu
410 415 420

tta tgg ccc aga gtg act tac cat caa ccc gaa tat gtg tac aca 1355
Leu Trp Pro Arg Val Thr Tyr His Gln Pro Glu Tyr Val Tyr Thr
425 430 435

cat ttt gcc aaa gct gtc agg ttc cga aga gaa cca ata tca cta 1400
His Phe Ala Lys Ala Val Arg Phe Arg Arg Glu Pro Ile Ser Leu
440 445 450

acg gtt gcc ctt atg ttg gga gga ctt act gta ggg ggc ata gcc 1445
Thr Val Ala Leu Met Leu Gly Gly Leu Thr Val Gly Gly Ile Ala
455 460 465

gcg ggg gtc gga aca ggg act aaa gcc ctc ctt gaa aca gcc cag 1490
Ala Gly Val Gly Thr Gly Thr Lys Ala Leu Leu Glu Thr Ala Gln
470 475 480

ttc aga caa cta caa atg gcc atg cac aca gac atc cag gcc cta 1535
Phe Arg Gln Leu Gln Met Ala Met His Thr Asp Ile Gln Ala Leu
485 490 495

gaa gaa tca att agt gcc tta gaa aag tcc ctg acc tcc ctt tct 1580
Glu Glu Ser Ile Ser Ala Leu Glu Lys Ser Leu Thr Ser Leu Ser
500 505 510

gaa gta gtc tta caa aac aga cgg ggc cta gat att cta ttc tta 1625
Glu Val Val Leu Gln Asn Arg Arg Glu Leu Asp Ile Leu Phe Leu
515 520 525

caa gag gga ggg ctc tgt gcc gca ttg aaa gaa gaa tgt tgc ttc 1670
Gln Glu Gly Gly Leu Cys Ala Ala Leu Lys Glu Glu Cys Cys Phe
530 535 540

tat gcg gat cac acc gga ctc gtc cga gac aat atg gcc aaa tta 1715
Tyr Ala Asp His Thr Gly Leu Val Arg Asp Asn Met Ala Lys Leu
545 550 555

aga gaa aga cta aaa cag cgg caa caa ctg ttt gac tcc caa cag 1760
Arg Glu Arg Leu Lys Gln Arg Gln Gln Leu Phe Asp Ser Gln Gln
560 565 570

gga tgg ttt gaa gga tgg ttc aac aag tcc ccc tgg ttt aca acc 1805
 Gly Trp Phe Glu Gly Trp Phe Asn Lys Ser Pro Trp Phe Thr Thr
 575 580 585

cta att tcc tcc att atg ggc ccc tta cta atc cta ctc cta att 1850
 Leu Ile Ser Ser Ile Met Gly Pro Leu Leu Ile Leu Leu Ile
 590 595 600

ctc ctc ttc ggc cca tgc atc ctt aac cga tta gta caa ttc gta
 1895 Leu Leu Phe Gly Pro Cys Ile Leu Asn Arg Leu Val Gln Phe
 Val
 605 610 615

aaa gac aga ata tct gtg gta cag gct tta att tta acc caa cag
 1940 Lys Asp Arg Ile Ser Val Val Gln Ala Leu Ile Leu Thr Gln
 Gln
 620 625 630

tac caa cag ata aag caa tac gat ccg gac cga cca tga 1979
 Tyr Gln Gln Ile Lys Gln Tyr Asp Pro Asp Arg Pro
 635 640

<210> 20

<211> 584

<212> PRT

<213> feline panleukopenia peritonitis virus

<220>

<223>

<400> 1

Met Ser Asp Gly Ala Val Gln Pro Asp Gly Gly Gln Pro Ala Val
 5 10 15

Arg Asn Glu Arg Ala Thr Gly Ser Gly Asn Gly Ser Gly Gly Gly
 20 25 30

Gly Gly Gly Gly Ser Gly Gly Val Gly Ile Ser Thr Gly Thr Phe
 35 40 45

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Asn	Asn	Gln	Thr	Glu	Phe	Lys	Phe	Leu	Glu	Asn	Gly	Trp	Val	Glu	
				50					55					60	
Ile	Thr	Ala	Asn	Ser	Ser	Arg	Leu	Val	His	Leu	Asn	Met	Pro	Glu	
				65					70					75	
Ser	Glu	Asn	Tyr	Lys	Arg	Val	Val	Val	Asn	Asn	Met	Asp	Lys	Thr	
				80					85					90	
Ala	Val	Lys	Gly	Asn	Met	Ala	Leu	Asp	Asp	Thr	His	Val	Gln	Ile	
				95					100					105	
Val	Thr	Pro	Trp	Ser	Leu	Val	Asp	Ala	Asn	Ala	Trp	Gly	Val	Trp	
				110					115					120	
Phe	Asn	Pro	Gly	Asp	Trp	Gln	Leu	Ile	Val	Asn	Thr	Met	Ser	Glu	
				125					130					135	
Leu	His	Leu	Val	Ser	Phe	Glu	Gln	Glu	Ile	Phe	Asn	Val	Val	Leu	
				140					145					150	
Lys	Thr	Val	Ser	Glu	Ser	Ala	Thr	Gln	Pro	Pro	Thr	Lys	Val	Tyr	
				155					160					165	
Asn	Asn	Asp	Leu	Thr	Ala	Ser	Leu	Met	Val	Ala	Leu	Asp	Ser	Asn	
				170					175					180	
Asn	Thr	Met	Pro	Phe	Thr	Pro	Ala	Ala	Met	Arg	Ser	Glu	Thr	Leu	
				185					190					195	
Gly	Phe	Tyr	Pro	Trp	Lys	Pro	Thr	Ile	Pro	Thr	Pro	Trp	Arg	Tyr	
				200					205					210	
Tyr	Phe	Gln	Trp	Asp	Arg	Thr	Leu	Ile	Pro	Ser	His	Thr	Gly	Thr	
				215					220					225	
Ser	Gly	Thr	Pro	Thr	Asn	Ile	Tyr	His	Gly	Thr	Asp	Pro	Asp	Asp	
				230					235					240	
Val	Gln	Phe	Tyr	Thr	Ile	Glu	Asn	Ser	Val	Pro	Val	His	Leu	Leu	
				245					250					255	
Arg	Thr	Gly	Asp	Glu	Phe	Ala	Thr	Gly	Thr	Phe	Phe	Phe	Asp	Cys	
				260					265					270	

Cys Pro Asn Asn Leu Val Val Glu Asp Glu Gly Cys Thr Asn
45 50 55

Leu Ser Gly Phe Ser Tyr Met Glu Leu Lys Val Gly Tyr Ile
60 65 70

Leu Ala Ile Lys Met Asn Gly Phe Thr Cys Thr Gly Val Val
75 80

Thr Glu Ala Glu Thr Tyr Thr Asn Phe Val Gly Tyr Val Thr
85 90 95

Thr Thr Phe Lys Arg Lys His Phe Arg Pro Thr Pro Asp Ala
100 105 110

Cys Arg Ala Ala Tyr Asn Trp Lys Met Ala Gly Asp Pro Arg
115 120 125

Tyr Glu Glu Ser Leu His Asn Pro Tyr Pro Asp Tyr Arg Trp
130 135 140

Leu Arg Thr Val Lys Thr Thr Lys Glu Ser Leu Val Ile Ile
145 150

Ser Pro Ser Val Ala Asp Leu Asp Pro Tyr Asp Arg Ser Leu
155 160 165

His Ser Arg Val Phe Pro Ser Gly Lys Cys Ser Gly Val Ala
170 175 180

Val Ser Ser Thr Tyr Cys Ser Thr Asn His Asp Tyr Thr Ile
185 190 195

Trp Met Pro Glu Asn Pro Arg Leu Gly Met Ser Cys Asp Ile
200 205 210

Phe Thr Asn Ser Arg Gly Lys Arg Ala Ser Lys Gly Ser Glu
215 220

Thr Cys Gly Phe Val Asp Glu Arg Gly Leu Tyr Lys Ser Leu
225 230 235

Lys Gly Ala Cys Lys Leu Lys Leu Cys Gly Val Leu Gly Leu
240 245 250

Ser Ala Gly Ala Leu Thr Ala Leu Met Leu Ile Ile Phe Leu
465 470 475

Met Thr Cys Cys Arg Arg Val Asn Arg Ser Glu Pro Thr Gln
480 485 490

His Asn Leu Arg Gly Thr Gly Arg Glu Val Ser Val Thr Pro
495 500

Gln Ser Gly Lys Ile Ile Ser Ser Trp Glu Ser His Lys Ser
505 510 515

Gly Gly Glu Thr Arg Leu
520 524

<210> 22

<211> 668

<212> PRT

<213> feline calicivirus

<220>

<223>

<400> 1

Met Cys Ser Thr Cys Ala Asn Val Leu Lys Tyr Tyr Asp Trp Asp
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Pro His Ile Lys Leu Val Ile Asn Pro Asn Lys Phe Leu His Val
20 25 30

Gly Phe Cys Asp Asn Pro Leu Met Cys Cys Tyr Pro Glu Leu Leu
35 40 45

Pro Glu Phe Gly Thr Met Trp Asp Cys Asp Gln Ser Pro Leu Gln
50 55 60

Val Tyr Leu Glu Ser Ile Leu Gly Asp Asp Glu Trp Ser Ser Thr
65 70 75

His	Glu	Ala	Ile	Asp	Pro	Val	Val	Pro	Pro	Met	His	Trp	Asp	Glu
				80						85				90
Ala	Gly	Lys	Ile	Phe	Gln	Pro	His	Pro	Gly	Val	Leu	Met	His	His
				95					100					105
Leu	Ile	Cys	Lys	Val	Ala	Glu	Gly	Trp	Asp	Pro	Asn	Leu	Pro	Leu
				110					115					120
Phe	Arg	Leu	Glu	Ala	Asp	Asp	Gly	Ser	Ile	Thr	Thr	Pro	Glu	Gln
				125					130					135
Gly	Thr	Met	Val	Gly	Gly	Val	Ile	Ala	Glu	Pro	Asn	Ala	Gln	Met
				140					145					150
Ser	Thr	Ala	Ala	Asp	Met	Ala	Thr	Gly	Lys	Ser	Val	Asp	Ser	Glu
				155					160					165
Trp	Glu	Ala	Phe	Phe	Ser	Phe	His	Thr	Ser	Val	Asn	Trp	Ser	Thr
				170					175					180
Ser	Glu	Thr	Gln	Gly	Lys	Ile	Leu	Phe	Lys	Gln	Ser	Leu	Gly	Pro
				185					190					195
Leu	Leu	Asn	Pro	Tyr	Leu	Thr	His	Leu	Ala	Lys	Leu	Tyr	Val	Ala
				200					205					210
Trp	Ser	Gly	Ser	Val	Asp	Val	Arg	Phe	Ser	Ile	Ser	Gly	Ser	Gly
				215					220					225
Val	Phe	Gly	Gly	Lys	Leu	Ala	Ala	Ile	Val	Val	Pro	Pro	Gly	Ile
				230					235					240
Asp	Pro	Val	Gln	Ser	Thr	Ser	Met	Leu	Gln	Tyr	Pro	His	Val	Leu
				245					250					255
Phe	Asp	Ala	Arg	Gln	Val	Glu	Pro	Val	Ile	Phe	Ser	Ile	Pro	Asp
				260					265					270
Leu	Arg	Ser	Thr	Leu	Tyr	His	Leu	Met	Ser	Asp	Thr	Asp	Thr	Thr
				275					280					285
Ser	Leu	Val	Ile	Met	Val	Tyr	Asn	Asp	Leu	Ile	Asn	Pro	Tyr	Ala
				290					295					300

Asn Asp Ser Asn Ser Ser Gly Cys Ile Val Thr Val Glu Thr Lys	305	310	315
Pro Gly Pro Asp Phe Lys Phe His Leu Leu Lys Pro Pro Gly Ser	320	325	330
Met Leu Thr His Gly Ser Ile Pro Ser Asp Leu Ile Pro Lys Ser	335	340	345
Ser Ser Leu Trp Ile Gly Asn Arg Phe Trp Ser Asp Ile Thr Asp	350	355	360
Phe Val Ile Arg Pro Phe Val Phe Gln Ala Asn Arg His Phe Asp	365	370	375
Phe Asn Gln Glu Thr Ala Gly Trp Ser Thr Pro Arg Phe Arg Pro	380	385	390
Ile Thr Ile Thr Ile Ser Val Lys Glu Ser Ala Lys Leu Gly Ile	395	400	405
Gly Val Ala Thr Asp Tyr Ile Val Pro Gly Ile Pro Asp Gly Trp	410	415	420
Pro Asp Thr Thr Ile Pro Gly Glu Leu Val Pro Val Gly Asp Tyr	425	430	435
Ala Ile Thr Asn Gly Thr Asn Asn Asp Ile Thr Thr Ala Ala Gln	440	445	450
Tyr Asp Ala Ala Thr Glu Ile Arg Asn Asn Thr Asn Phe Arg Gly	455	460	465
Met Tyr Ile Cys Gly Ser Leu Gln Arg Ala Trp Gly Asp Lys Lys	470	475	480
Ile Ser Asn Thr Ala Phe Ile Thr Thr Gly Thr Val Asp Gly Ala	485	490	495
Lys Leu Ile Pro Ser Asn Thr Ile Asp Gln Thr Lys Ile Ala Val	500	505	510
Phe Gln Asp Thr His Ala Asn Lys His Val Gln Thr Ser Asp Asp	515	520	525

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1	5	10	15
Tyr Gly Glu Arg	Tyr Cys Ala Met	Gln Asp Ser Gly	Leu Gln Cys
	20	25	30
Ile Gln Gly Thr	Gln Ser Arg Cys	Gln Thr Cys Phe	Glu Arg Gly
	35	40	45
Asp Leu Ile Trp	His Leu Ala Asn	Trp Asn Phe Ser	Trp Ser Val
	50	55	60
Ile Leu Ile Val	Phe Ile Thr Val	Leu Gln Tyr Gly	Arg Pro Gln
	65	70	75
Phe Ser Trp Leu	Val Tyr Gly Ile	Lys Met Leu Ile	Met Trp Leu
	80	85	90
Leu Trp Pro Ile	Val Leu Ala Leu	Thr Ile Phe Asn	Ala Tyr Ser
	95	100	105
Glu Tyr Gln Val	Ser Arg Tyr Val	Met Phe Gly Phe	Ser Val Ala
	110	115	120
Gly Ala Val Val	Thr Phe Ala Leu	Trp Met Met Tyr	Phe Val Arg
	125	130	135
Ser Val Gln Leu	Tyr Arg Arg Thr	Lys Ser Trp Trp	Ser Phe Asn
	140	145	150
Pro Glu Thr Asn	Ala Ile Leu Cys	Val Asn Ala Leu	Gly Arg Ser
	155	160	165
Tyr Val Leu Pro	Leu Asp Gly Thr	Pro Thr Gly Val	Thr Leu Thr
	170	175	180
Leu Leu Ser Gly	Asn Leu Tyr Ala	Glu Gly Phe Lys	Met Ala Gly
	185	190	195
Gly Leu Thr Ile	Glu His Leu Pro	Lys Tyr Val Met	Ile Ala Thr
	200	205	210
Pro Ser Arg Thr	Ile Val Tyr Thr	Ile Val Gly Lys	Gln Leu Lys
	215	220	225
Ala Thr Thr Ala	Thr Gly Trp Ala	Tyr Tyr Val Lys	Ser Lys Ala

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230	235	240
Gly Asp Tyr Ser Thr Glu Ala Arg Thr	Asp Asn Leu Ser Glu His	
245	250	255
Glu Lys Leu Leu His Met Val		
260		
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<211> 377		
<212> PRT		
<213> feline infectious peritonitis virus		
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<223>		
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Met Ala Thr Gln Gly Gln Arg Val Asn Trp Gly Asp Glu Pro Ser		
1	5	10 15
Lys Arg Arg Gly Arg Ser Asn Ser Arg Gly Arg Lys Asn Asn Asp		
20	25	30
Ile Pro Leu Ser Phe Tyr Asn Phe Ile Thr Leu Glu Gln Glu Ser		
35	40	45
Lys Phe Trp Asn Leu Cys Pro Arg Asp Leu Val Pro Lys Gly Ile		
50	55	60
Gly Asn Lys Asp Gln Gln Ile Gly Tyr Trp Asn Arg Gln Ile Arg		
65	70	75
Tyr Arg Ile Val Lys Gly Gln Arg Lys Glu Leu Ala Glu Arg Trp		
80	85	90

Phe Phe Tyr Phe Leu Gly Thr Gly Phe His Ala Asp Ala Lys Phe
 95 100 105

Lys Asp Lys Ile Asp Gly Val Phe Trp Val Ala Arg Asp Gly Ala
 110 115 120

Met Asn Lys Pro Thr Thr Leu Gly Thr Arg Gly Thr Asn Asn Glu
 125 130 135

Ser Lys Pro Leu Arg Phe Asp Gly Lys Ile Pro Pro Gln Phe Gln
 140 145 150

Leu Glu Val Asn Arg Ser Arg Asn Asn Ser Arg Ser Gly Ser Gln
 155 160 165

Ser Arg Ser Val Ser Arg Asn Arg Ser Gln Ser Arg Gly Arg His
 170 175 180

His Ser Asn Asn Gln Asn Asn Asn Val Glu Asp Thr Ile Val Ala
 185 190 195

Val Leu Glu Lys Leu Gly Val Thr Asp Lys Gln Arg Ser Arg Ser
 200 205 210

Lys Pro Arg Glu Arg Ser Asp Ser Lys Pro Arg Asp Thr Thr Pro
 215 220 225

Lys Asn Ala Asn Lys His Thr Trp Lys Lys Thr Ala Gly Lys Gly
 230 235 240

Asp Val Thr Thr Phe Tyr Gly Ala Arg Ser Ser Ser Ala Asn Phe
 245 250 255

Gly Asp Ser Asp Leu Val Ala Asn Gly Asn Ala Ala Lys Cys Tyr
 260 265 270

Pro Gln Ile Ala Glu Cys Val Pro Ser Val Ser Ser Ile Ile Phe
 275 280 285

Gly Ser Gln Trp Ser Ala Glu Glu Ala Gly Asp Gln Val Lys Val
 290 295 300

Thr Leu Thr His Thr Tyr Tyr Leu Pro Lys Asp Asp Ala Lys Thr
 305 310 315

Ser Gln Phe Leu Glu Gln Ile Asp Ala Tyr Lys Atg Pro Ser Glu
 320 325 330

Val Ala Lys Asp Gln Arg Gln Arg Arg Ser Arg Ser Lys Ser Ala
 335 340 345

Asp Lys Lys Pro Glu Glu Lys Ser Val Thr Leu Val Glu Ala Tyr
 350 355 360

Thr Asp Val Phe Asp Asp Thr Gln Val Glu Met Ile Asp Glu Val
 365 370 375

Thr Asn
 377

<210> 25

<211> 642

<212> PRT

<213> feline leukemia virus

<220>

<223>

<400> 1

Met	Glu	Ser	Pro	Thr	His	Pro	Lys	Pro	Ser	Lys	Asp	Lys	Thr	Leu
1				5					10					15
Ser	Trp	Asn	Leu	Ala	Phe	Leu	Val	Gly	Ile	Leu	Phe	Thr	Ile	Asp
			20						25					30
Ile	Gly	Met	Ala	Asn	Pro	Ser	Pro	His	Gln	Ile	Tyr	Asn	Val	Thr
			35						40					45
Trp	Val	Ile	Thr	Asn	Val	Gln	Thr	Asn	Thr	Gln	Ala	Asn	Ala	Thr
				50					55					60
Ser	Met	Leu	Gly	Thr	Leu	Thr	Asp	Ala	Tyr	Pro	Thr	Leu	His	Val
				65					70					75
Asp	Leu	Cys	Asp	Leu	Val	Gly	Asp	Thr	Trp	Glu	Pro	Ile	Val	Leu
				80					85					90
Asn	Pro	Thr	Asn	Val	Lys	His	Gly	Ala	Arg	Tyr	Ser	Ser	Ser	Lys
				95					100					105
Tyr	Gly	Cys	Lys	Thr	Thr	Asp	Arg	Lys	Lys	Gln	Gln	Gln	Thr	Tyr
				110					115					120
Pro	Phe	Tyr	Val	Cys	Pro	Gly	His	Ala	Pro	Ser	Leu	Gly	Pro	Lys
				125					130					135
Gly	Thr	His	Cys	Gly	Gly	Ala	Gln	Asp	Gly	Phe	Cys	Ala	Ala	Trp
				140					145					150
Gly	Cys	Glu	Thr	Thr	Gly	Glu	Thr	Trp	Trp	Lys	Pro	Thr	Ser	Ser
				155					160					165
Trp	Asp	Tyr	Ile	Thr	Val	Lys	Arg	Gly	Ser	Ser	Gln	Asp	Asn	Ser
				170					175					180
Cys	Glu	Gly	Lys	Cys	Asn	Pro	Leu	Val	Leu	Gln	Phe	Thr	Gln	Lys
				185					190					195
Gly	Arg	Gln	Ala	Ser	Trp	Asp	Gly	Pro	Lys	Met	Trp	Gly	Leu	Arg
				200					205					210

Leu Tyr Arg Thr	Gly Tyr Asp Pro Ile	Ala Leu Phe Thr Val Ser
215	220	225
Arg Gln Val Ser	Thr Ile Thr Pro Pro	Gln Ala Met Gly Pro Asn
230	235	240
Leu Val Leu Pro	Asp Gln Lys Pro Pro	Ser Arg Gln Ser Gln Thr
245	250	255
Gly Ser Lys Val	Ala Thr Gln Arg Pro	Gln Thr Asn Glu Ser Ala
260	265	270
Pro Arg Ser Val	Ala Pro Thr Thr Met	Gly Pro Lys Arg Ile Gly
275	280	285
Thr Gly Asp Arg	Leu Ile Asn Leu Val	Gln Gly Thr Tyr Leu Ala
290	295	300
Leu Asn Ala Thr	Asp Pro Asn Lys Thr	Lys Asp Cys Trp Leu Cys
305	310	315
Leu Val Ser Arg	Pro Pro Tyr Tyr Glu	Gly Ile Ala Ile Leu Gly
320	325	330
Asn Tyr Ser Asn	Gln Thr Asn Pro Pro	Pro Ser Cys Leu Ser Ile
335	340	345
Pro Gln His Lys	Leu Thr Ile Ser Glu	Val Ser Gly Gln Gly Met
350	355	360
Cys Ile Gly Thr	Val Pro Lys Thr His	Gln Ala Leu Cys Asn Lys
365	370	375
Thr Gln Gln Gly	His Thr Gly Ala His	Tyr Leu Ala Ala Pro Asn
380	385	390
Gly Thr Tyr Trp	Ala Cys Asn Thr Gly	Leu Thr Pro Cys Ile Ser
395	400	405
Met Ala Val Leu	Asn Trp Thr Ser Asp	Phe Cys Val Leu Ile Glu
410	415	420
Leu Trp Pro Arg	Val Thr Tyr His Gln	Pro Glu Tyr Val Tyr Thr
425	430	435

His Phe Ala Lys	Ala Val Arg Phe Arg	Axg Glu Pro Ile Ser Leu	
	440	445	450
Thr Val Ala Leu	Met Leu Gly Gly Leu	Thr Val Gly Gly Ile Ala	
	455	460	465
Ala Gly Val Gly	Thr Gly Thr Lys Ala	Leu Leu Glu Thr Ala Gln	
	470	475	480
Phe Arg Gln Leu	Gln Met Ala Met His	Thr Asp Ile Gln Ala Leu	
	485	490	495
Glu Glu Ser Ile	Ser Ala Leu Glu Lys	Ser Leu Thr Ser Leu Ser	
	500	505	510
Glu Val Val Leu	Gln Asn Arg Arg Glu	Leu Asp Ile Leu Phe Leu	
	515	520	525
Gln Glu Gly Gly	Leu Cys Ala Ala Leu	Lys Glu Glu Cys Cys Phe	
	530	535	540
Tyr Ala Asp His	Thr Gly Leu Val Arg	Asp Asn Met Ala Lys Leu	
	545	550	555
Arg Glu Arg Leu	Lys Gln Arg Gln Gln	Leu Phe Asp Ser Gln Gln	
	560	565	570
Gly Trp Phe Glu	Gly Trp Phe Asn Lys	Ser Pro Trp Phe Thr Thr	
	575	580	585
Leu Ile Ser Ser	Ile Met Gly Pro Leu	Leu Ile Leu Leu Leu Ile	
	590	595	600
Leu Leu Phe Gly	Pro Cys Ile Leu Asn Arg	Leu Val Gln Phe Val	
	605	610	615
Lys Asp Axg Ile	Ser Val Val Gln Ala	Leu Ile Leu Thr Gln Gln	
	620	625	630
Tyr Gln Gln Ile	Lys Gln Tyr Asp Pro	Asp Arg Pro	
	635	640	